



A1

SEQUENCE LISTING

<110> LEUNG, Shui On
HANSEN, Hans

<120> IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
AND LEUKEMIA CELLS

<130> 018733/1082

<140> US 09/988,013
<141> 2001-11-16

<150> US 09/741,843
<151> 2000-12-22

<150> US 09/127,902
<151> 1998-08-03

<150> US 08/690,102
<151> 1996-07-06

<150> US 08/289,576
<151> 1994-08-12

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<170> PatentIn version 3.1

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<220>
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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

| | |
|---|-----|
| atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa | 288 |
| Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln | |
| 85 90 95 | |

| | |
|---|-----|
| tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa | 336 |
| Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys | |
| 100 105 110 | |

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| cgt | 339 |
| Arg | |

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| 1 5 10 15 |

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|---|
| Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser |
| 20 25 30 |

| |
|---|
| Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln |
| 35 40 45 |

| |
|---|
| Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val |
| 50 55 60 |

| |
|---|
| Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr |
| 65 70 75 80 |

| |
|---|
| Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln |
| 85 90 95 |

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| Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys |
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Arg

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Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
1 5 10 15
tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144
Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60
aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336
Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110
aca gtc tcc tcg 348
Thr Val Ser Ser
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1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa 144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc 240
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa 288
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
85 90 95

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa 336
Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
100 105 110

cgt 339
Arg

<210> 6
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<212> PRT
<213> Homo sapiens

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Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
100 105 110

Arg

<210> 7

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att 144
Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

| | |
|---|-----|
| aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac | 240 |
| Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr | |
| 65 70 75 80 | |

| | |
|---|-----|
| atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt | 288 |
| Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys | |
| 85 90 95 | |

| | |
|---|-----|
| gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc | 336 |
| Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val | |
| 100 105 110 | |

| | |
|-----------------|-----|
| acc gtc tcc tcg | 348 |
| Thr Val Ser Ser | |
| 115 | |

<210> 8
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<400> 8

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|---|
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| 1 5 10 15 |

| |
|---|
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr |
| 20 25 30 |

| |
|---|
| Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile |
| 35 40 45 |

| |
|---|
| Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe |
| 50 55 60 |

| |
|---|
| Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr |
| 65 70 75 80 |

| |
|---|
| Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys |
| 85 90 95 |

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|---|
| Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val |
| 100 105 110 |

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|-----------------|
| Thr Val Ser Ser |
| 115 |

<210> 9
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
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ctgatgaccc aggtttcttg acttcagcc 149

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<211> 134

<212> DNA

<213> Unknown

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 ttgaagttct gatt 134

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<210> 13
 <211> 33
 <212> DNA
 <213> Unknown
 <220>
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<210> 14
 <211> 49
 <212> DNA
 <213> Unknown
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<210> 15
 <211> 44
 <212> DNA
 <213> Unknown
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<400> 15
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<210> 16
 <211> 150
 <212> DNA
 <213> Unknown
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ggccaagtag ttcttgtgat ttgcactgta taaaacactt tgactggact tacagctcat 120
agtgacccta tctccaacag atgcgctcag 150

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<211> 52
<212> DNA
<213> Unknown
<220>
<223> primer

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<210> 18
<211> 45
<212> DNA
<213> Unknown
<220>
<223> primer

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<210> 19
<211> 121
<212> DNA
<213> Unknown
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<400> 19
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caatgtcttc tggttgaaga gagctgatgg tgaaagtaaa atctgtccca gatccgctgc 120
c 121

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<212> DNA
<213> Unknown
<220>
<223> primer

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<210> 21
<211> 33
<212> DNA
<213> Unknown
<220>
<223> primer

<400> 21
gaccggcaga tctgcacctt ggtccctcca ccg

33

A' Coral
